Using genome-wide predictions in a functional-structural plant model to simulate the genetic variation of 1-year-old apple tree development under contrasted soil water conditions

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Context

A large genetic variability in tree architecture has been observed in bi-parental apple tree populations (Segura et al., 2006)

QTLs related to architectural traits have been identified (Segura et al., 2008).

These genotypic effets have not been integrated in the apple tree FSPM, MappleT (Costes et al. 2008).

Fig 1. *Architecture variability in the Starkimson x Granny F1 progeny*

General objective: integrating genetic control in MAppleT

Material and methods

Modelling phyllochron and probabilities of sylleptic branching

Four new parameters (Table 1) with major impact on the first year of growth were included in MAppleT.

The rate of leaf emergence (RLE_{GDD}) was assumed to depend on the thermal time (Lescourret et al. 1998)

Table 1. *New parameters of MAppleT*

Process	Parameter name	Parameter definition	Units
Leaf emergence	*RLEGDD*	Rate of leaf emergence depending on temperature	GDD
Sylleptic branching	a_{syll}	Probability of emergence of sylleptic branches	GDD^{-1}
Individual internode elongation	IN_length	Final internode length	cm
Individual leaf expansion	Leaf_area	Final leaf area	cm^2

Sylleptic branching probability (P_{syll}) was assumed to depend on the rate of leaf emergence during the season (Peyrhardi et al. 2013)

Main equations used to simulate genotypic effects

$$RLE(t) = RLE_{GDD} \times T_{eff}(t)$$

$$P_{syll}(t) = a_{syll}\left(\frac{1}{n_{days}}\sum_{i=t-n_{days}}^{t} RLE_i\right) \times RLE(t)$$

Model calibration and genome wide prediction

Parameter values (RLE_{Gdd} , a_{syll} , IN_length, Leaf_area) were estimated on 116 genotypes of the bi-parental ('Starkimson' x 'Granny Smith') population, observed in 2007.

Genotyping allowed detecting 3123 SNPs polymorphisms that were used for genome wide predictions.

Genome wide prediction was performed using Ridge Regression Blups (Endelman, 2011; Fodor et al. 2013).

Marker effects were evaluated using a mixed effect model assuming infintisemial effects.

$$Y = \mu + Xg + e \quad with \quad g \sim N(0, I_n\sigma_g^2)$$

Vector of model parameters

$$\begin{pmatrix} Y_1 \\ Y_2 \\ \vdots \\ Y_n \end{pmatrix}$$

$$\begin{pmatrix} -1 & 1 & -1 & 1 & \cdots & -1 & 1 \\ -1 & 1 & 1 & -1 & \cdots & 1 & 1 \\ \vdots & \vdots & & \ddots & & \vdots & \\ 1 & -1 & 1 & 1 & \cdots & -1 & 1 \end{pmatrix}$$

Matrix of genotypes at each marker

$$\begin{pmatrix} g_1 \\ g_2 \\ \vdots \\ g_n \end{pmatrix}$$

Vector of markers effects

Model simulation and validation

When running simulations, values of MAppleT parameters were estimated using the genetic information provided by the genome wide prediction model.

The quality of simulations was assessed by comparing model simulations and observations of integrative plant variables (trunk length, number of sylleptics) in 2007 and under independant climatic conditions in 2004.

Results

Simulations of phenotypic variability

The MAppleT model simulated large range of 1-year-old apple tree phenotypes (Fig. 2).

Correlations between simulated traits (trunk length, number of branches, number of leaves) were consistent with the correlations for the observed traits (Table 2), suggesting independant genetics controls.

Table 2. *Correlations between architectural traits for observations and simulations*

	Nb_Leaves	Trunk length	Nb_Syll
Nb_Leaves		0.34	0.26
Trunk length	0.41		-0.09
Nb_Syll	0.25	-0.03	

Correlations from observed data

Correlations from simulated data

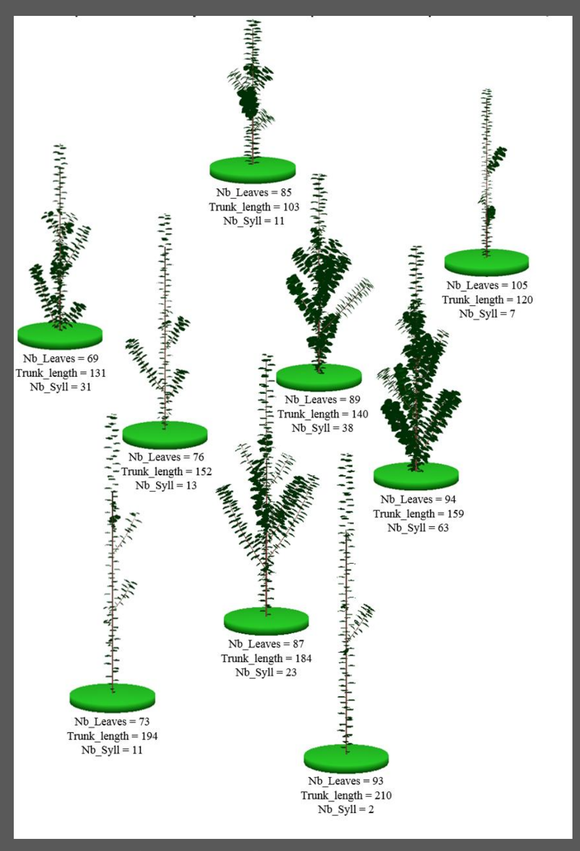

Fig 2. *Graphical outputs of MAppleT simulations for nine apple tree genotypes with contrasted architecture*

Model validation on integrative traits

High correlations and low RMSE between observations and simulations were found for the simulations of integrative traits in 2007 (Fig. 3).

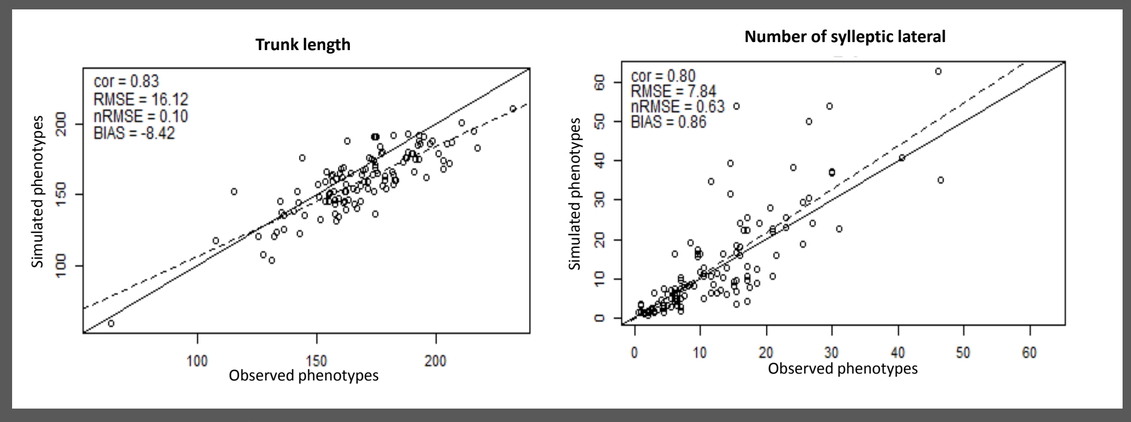

Fig 3. *Comparison of observed and simulated phenotypes in 2004*.

Model validation under independant climatic conditions

Under environmental conditions not used for model calibration (year 2004), correlations between simulated and observed values were lower (Fig. 4).

The environmental effects presently included in MAppleT, i.e. temperature effect on the phyllochrone and sylleptic branching, are not sufficient to correctly simulate the GxE interactions.

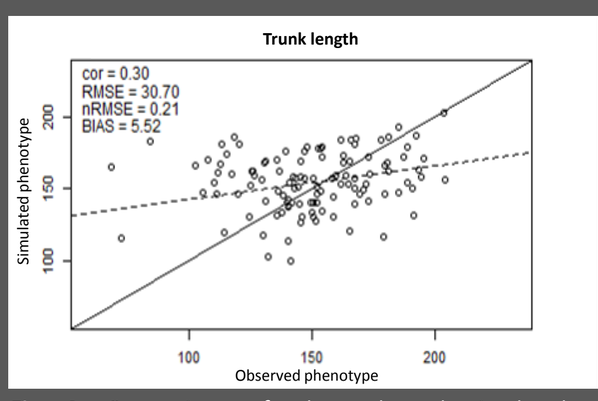

Fig 4. *Comparison of observed and simulated phenotypes in 2004*

Conclusions

This study corresponds to a first attempt to introduce genome-wide information in a FSPM for a fruit tree.

Even though futher improvements are required to better model genotype x environment interactions, it opens new possibilities for supporting plant breeding by *in-silico* evaluations of the impact of genotypic polymorphisms on integrative phenotypes.

References

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